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(21) International Application Number: PCT/US99/12461 (22) International Filing Date: 04 June 1999 (04.06.1999) (60) Parent Application or Grant LIN, Shi-Lung [/]; (). YING, Shao-Yao [/]; (). CHUONG, Cheng-Ming [/]; (). WIDELITZ, Randall, Bruce [/]; (). LIN, Shi-Lung [/]; (). YING, Shao-Yao [/]; (). CHUONG, Cheng-Ming [/]; (). WIDELITZ, Randall, Bruce [/]; (). CHAN, Raymond; ().	Published	
(54) Title: RNA POLYMERASE CHAIN REACTION (54) Titre: AMPLIFICATION EN CHAÎNE D'ARN PAR POLYMERASE		
(57) Abstract <p>The present invention provides a fast, simple and specific method for generating amplified messenger RNAs from limited messenger RNAs. The principle of this RNA-polymerase chain reaction method relies upon the cycling steps of reverse transcription, denaturation, double-stranded cDNA synthesis and then in vitro transcription to bring up the amount of messenger RNAs to two thousand folds within one round of above procedure. This method is primarily designed for differential screening of tissue-specific gene expressions in cell level, cloning full-length sequences of unknown gene transcripts, generating probes for hybridization assays, synthesizing peptides in vitro, and preparing representative cDNAs for modern gene chip technology. In conjunction with a cell fixation and permeabilisation step, a complete full-length cDNA library can be directly generated from few single cells without mRNA degradation.</p> (57) Abrégé <p>La présente invention concerne une méthode rapide, simple et spécifique de production d'ARN messagers amplifiés à partir d'ARN messagers limités. Le principe de cette méthode d'amplification en chaîne d'ARN par polymérase se base sur les étapes cycliques de la transcription inverse, dénaturation, synthèse d'ADNc bicaténaire et ensuite la transcription in vitro afin d'élever la quantité d'ARN messagers de 2000 fois en un cycle de la procédure précitée. Cette méthode est conçue essentiellement pour le criblage différentiel d'expressions de gènes à spécificité tissulaire au niveau cellulaire, le clonage de séquence de longueur totale de transcrits de gène inconnu, la production de sondes destinées à des dosages d'hybridation, la synthèse de peptides in vitro et la préparation d'ADNc représentatif pour la technologie moderne des puces à ADN. Simultanément à une étape de fixation et de perméabilisation cellulaire, une banque d'ADNc de longueur totale complète peut être générée directement à partir de quelques cellules individuelles sans dégradation de l'ARNm.</p>		

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(54) Title: RNA POLYMERASE CHAIN REACTION

(57) Abstract: The present invention provides a fast, simple and specific method for generating amplified messenger RNAs from limited messenger RNAs. The principle of this RNA-polymerase chain reaction method relies upon the cycling steps of reverse transcription, denaturation, double-stranded cDNA synthesis and then in vitro transcription to bring up the amount of messenger RNAs to two thousand folds within one round of above procedure. This method is primarily designed for differential screening of tissue-specific gene expressions in cell level, cloning full-length sequences of unknown gene transcripts, generating probes for hybridization assays, synthesizing peptides in vitro, and preparing representative cDNAs for modern gene chip technology. In conjunction with a cell fixation and permeabilisation step, a complete full-length cDNA library can be directly generated from few single cells without mRNA degradation.

Description

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RNA POLYMERASE CHAIN REACTION

BACKGROUND OF THE INVENTION

1. Field of the Invention

The present invention generally relates to the field of methods for generating amplified messenger RNA sequences. More particularly, the present invention relates to the field of polymerase chain reaction methods of messenger RNA amplification from single cells.

2. Description of the Prior Art

The following references are pertinent to this invention:

1. Sambrook et.al., "*Molecular Cloning, 2nd Edition*", Cold Spring Harbor Laboratory Press, pp8.11-8.19 (1989).
2. Van Gelder et.al., "Amplified RNA synthesized from limited quantities of heterogeneous cDNA", *Proc. Natl. Acad. Sci. USA* 87: 1663-1667 (1990).
3. O'Dell et.al., "Amplification of mRNAs from Single, Fixed, TUNEL-Positive Cells", *BioTechniques* 25: 566-570 (1998).

4. Eberwine et.al. , "Analysis of gene expression in single live neurons",
Proc. Natl. Acad. Sci. USA 89: 3010-3014 (1992).
5. Crino et.al., "Embryonic neuronal markers in tuberous sclerosis: Single-
Cell Molecular Pathology", *Proc. Natl. Acad. Sci. USA* 93: 14152-14157
(1996).
6. Embleton et.al., "In-cell PCR from mRNA: amplifying and linking the
rearranged immunoglobulin heavy and light chain V-genes within single
cells", *Nucleic Acid Res.* 20: 3831-3837 (1992).
7. United States Patent No. 4,683,202 issued to Mullis et.al.
8. United States Patent No. 5,817,465 issued to Mallet et.al.
9. United States Patent No. 5,514,545 issued to Eberwine et.al.

The ability to amplify messenger RNAs (mRNA) directly from single cells has permitted the molecular investigations of intracellular gene expressions under certain special conditions, such as pathogenesis, mutation, treatment processing and developmental control. In general, mRNAs are reverse-transcribed to complementary DNAs (cDNA) for preventing degradation. Because the integrity and quantity of mRNAs determine the completeness of a full-length cDNA library, the acquirement of large amount of high quality mRNAs from single cells is the major problem in the sample preparations of various genetic research. Especially, when mRNAs from single cells of a special tissue are used to generate a cDNA library, the library must contain intact gene expression pattern in order to identify tissue-specific genes differentially expressed in vivo. Although previous methods for cDNA library synthesis (Sambrook et.al., "*Molecular Cloning, 2nd Edition*", pp8.11-8.35 (1989)) have succeeded in generating full-length cDNAs, the tedious procedures of reverse transcription, restriction, adaptor ligation and vector cloning usually fail to maintain the completeness

5 of mRNA sequences, resulting in loss of rare representative cDNAs when limited cells are used.

10 On the other hand, the amplification of RNA-related cDNAs by reverse transcription-polymerase chain reaction (RT-PCR) has become the most common way among current RNA amplification methods. Prior art attempts at amplifying RNAs with RT-PCR, such as United States Patent No. 4,683,202 to Mullis and United States
15 Patent No. 5,817,465 to Mallet, uses mRNA templates to multiply respective cDNAs. Although the RT-PCR methods successfully increase the quantity of double-stranded cDNAs from respective RNAs, the fidelity of resulting cDNAs is not completely
20 identical to their RNA origins due to the mis-reading nature of polymerase chain reaction (PCR). Moreover, the final products of RT-PCR are double-stranded DNAs, rather than mRNAs, which can not be used in probe hybridization and in vitro
25 translation. Furthermore, current RT-PCR methods are not designed for the amplification of full-length mRNAs or cDNAs, indicating the impossibility of generating a full-length cDNA library by this method. Those disadvantages exclude the
30 use of RT-PCR in the analysis of screening unknown gene expressions.

The generation of amplified anti-sense RNAs (aRNA) has been developed to increase transcriptional copies of specific mRNAs from single cells (Van Gelder et.al.,
35 *Proc. Natl. Acad. Sci. USA* 87: 1663-1667 (1990)). The aRNA can be used for characterization of the cellular expression pattern of certain genes, but not all (O'Dell et.al., *BioTechniques* 25: 566-570 (1998)). Prior art attempts at aRNA amplification, such as United States Patent No. 5,514,545 to Eberwine, uses the amplified aRNAs as
40 probes for potential diagnosis and therapy. By incorporating a poly(dT) primer coupled to a T7 RNA polymerase promoter sequence, named oligo(dT)-promoter, during reverse transcription (RT), the single copy mRNA can be amplified up to two thousand
45 folds by one round of aRNA amplification (Eberwine et.al., *Proc. Natl. Acad. Sci. USA* 89: 3010-3014 (1992)). The aRNAs prepared from single live neuron has been reported to cover 50-75% of total intracellular mRNA population (Eberwine et.al., (1992); Crino
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5 et.al., *Proc. Natl. Acad. Sci. USA* 93: 14152-14157 (1996)), indicating that the
prevention of RNA degradation in cells is required to achieve 100% coverage of mRNA
10 amplification. Although these aRNA synthesis methods lead to the identification of
some abundant mRNA markers from single cells, the rare mRNAs may not be
assessable by the current aRNA methods (O'Dell et.al. (1998)), resulting in low
completeness of aRNAs. On the other hand, what aRNA amplification method does is
15 generation of "anti-sense" RNAs, rather than that of mRNAs which are of sense
conformation.

20 In summary, it is desirable to have a fast, simple and specific method for
generating amplifiable mRNAs from single cells, of which the results may be applied to
screen differentially expressed genes, to search functional domains for gene regulation,
to produce synthetic peptides in vitro, and even to design a therapy for diseases.

25 SUMMARY OF THE INVENTION

30 The present invention is a novel polymerase chain reaction method which
amplifies messenger RNAs from single cells.

35 Described in detail, a preferred embodiment of the present invention method
includes the following steps:

- 40
- a. preventing a plurality of messenger RNAs from degradation, wherein said
messenger RNAs are protected to be intact along with following steps;
 - 45 b. contacting said messenger RNAs with a plurality of
oligodeoxythymidylate nucleotide sequences to form a plurality of first-
strand complementary DNAs, wherein said first-strand complementary
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DNAs are generated by reverse transcription of said messenger RNAs with said oligodeoxythymidylate nucleotide sequences as primer;

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- c. permitting 3'-end extension of said first-strand complementary DNAs to form a plurality of polynucleotide-tailed first-strand complementary DNAs, wherein said polynucleotide-tailed first-strand complementary DNAs are extended by terminal transferase activity with multiple copies of same deoxynucleotides to form polynucleotide tails;

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- d. incubating denatured said polynucleotide-tailed first-strand complementary DNAs with a plurality of oligo(anti-sense polynucleotide)-promoter primers to form a plurality of double-stranded complementary DNAs, wherein said double-stranded complementary DNAs are generated by extension of DNA polymerase activity with said oligo(anti-sense polynucleotide)-promoter primers complementary to the polynucleotide tails of said polynucleotide-tailed first-strand complementary DNAs;

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- e. permitting transcription of said double-stranded complementary DNAs to form a plurality of amplified messenger RNAs, wherein said amplified messenger RNAs are generated by extension of RNA polymerase activity through the promoter region of said double-stranded complementary DNAs; and

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- f. contacting said amplified messenger RNAs with said oligodeoxythymidylate nucleotide sequences to form a plurality of said polynucleotide-tailed first-strand complementary DNAs, wherein said polynucleotide-tailed first-strand complementary DNAs are generated by reverse transcription of said amplified messenger RNAs with said oligodeoxythymidylate nucleotide sequences as primer.

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5 In one aspect of this embodiment, the cycling steps of (d) through (f) can be repeated at least one time for the amplification of said messenger RNAs. According to another aspect of this preferred embodiment, the final nucleotide products are preserved
10 in the form of double-stranded duplexes to prevent the degradation of amplified messenger RNAs, preferably, in the form of RNA-DNA hybrid duplexes in the step (f).

15 The mRNAs can be prepared from a plurality of fixed cells, wherein said fixed cells are protected from RNA degradation and also subjected to permeabilisation for enzyme penetration. Those fixed cells include fixative-treated cultural cells, frozen fresh tissues, fixative-treated fresh tissues or paraffin-embedded tissues on slides. To
20 increase the transcriptional production of mRNAs in the step (e), the promoter sequences are preferably incorporated into the 5'-ends of said second-strand cDNAs. In another aspect of this embodiment, said amplified mRNAs are preferably capped by P¹-5'-(7-methyl)-guanosine-P³-5'-adenosine-triphosphate or P¹-5'-(7-methyl)-guanosine-P³-5'-guanosine-triphosphate in the step (e) for further in vitro translation. On the other
25 hand, the deoxynucleotide used in the tailing reaction of said first-strand complementary DNAs is either deoxyguanylate (dG) or deoxycytidylate (dC), and the average number of tailed nucleotides is larger than seven; most preferably, the number is about twelve. Advantageously, the final amplified mRNAs can be continuously
30 reverse-transcribed into double-stranded cDNA by Tth-like DNA polymerase activity. The final double-stranded cDNAs are preferably cloned into competent vectors for further applications, such as transfection assay, differential screening, functional
35 detection and so on.
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45 Further novel features and other objects of the present invention will become apparent from the following detailed description, discussion and the appended claims, taken in conjunction with the drawings.

BRIEF DESCRIPTION OF THE DRAWINGS

Referring particularly to the drawings for the purpose of illustration only and not limitation, there is illustrated:

FIG.1 is an illustration of the preferred embodiment of RNA-polymerase chain reaction of the subject invention;

FIG.2 is an illustration of second preferred embodiment of RNA-polymerase chain reaction of the subject invention;

FIG.3 is an illustration of third preferred embodiment of the RNA-polymerase chain reaction of the subject invention; and

FIGS.4a-4b is the result of example 4 of the subject invention.

DESCRIPTION OF THE PREFERRED EMBODIMENT

Although specific embodiments of the present invention will now be described with reference to the drawings, it should be understood that such embodiments are by way of example only and merely illustrative of but a small number of the many possible specific embodiments which can represent applications of the principles of the present invention. Various changes and modifications obvious to one skilled in the art to which the present invention pertains are deemed to be within the spirit, scope and contemplation of the present invention as further defined in the appended claims.

The present invention is directed to a novel polymerase chain reaction method for mRNA amplification from single cells, named "RNA-polymerase chain reaction (RNA-PCR)". This method is primarily designed for differential screening of tissue-

5 specific gene expressions in cell level, cloning full-length sequences of unknown gene
transcripts, generating pure probes for hybridization assays, synthesizing peptides in
vitro, and preparing complete cDNA libraries for gene chip technology. The purpose of
10 the RNA-PCR relies on the repeating steps of reverse transcription, denaturation,
double-stranded cDNA synthesis and in vitro transcription to bring up the population of
mRNAs to two thousand folds in one cycle of above procedure. In brief, the preferred
15 version (FIG.1) of the present invention is based on: 1) prevention of mRNA
degradation, 2) first reverse transcription and terminal transferase reaction to
incorporate 3'-polynucleotide tails to the first-strand cDNAs, 3) denaturation and then
double-stranded cDNA formation based on the extension of specific promoter-primers
20 complementary to the 3'-polynucleotide tails, 4) transcription from promoter to amplify
mRNAs up to two thousand folds per round, and 5) repeating aforementioned steps to
achieve desired RNA amplification.

Alternatively, the second preferred version (FIG.2) of the present invention is
based on: 1) prevention of mRNA degradation, 2) first reverse transcription to
30 incorporate first promoters to the 5'-ends of first-strand cDNAs and then addition of
polynucleotide sequences to the 3'-ends of the first-strand cDNAs, 3) double-stranded
cDNA synthesis based on the extension of second promoter sequences complementary
35 to the 3'-polynucleotide regions of the first-strand cDNAs, 4) transcription to amplify
either aRNAs or mRNAs up to two thousand folds in the first round of amplification
cycle, and 5) repeating aforementioned cycling steps to achieve desired amount of
RNAs. As shown in FIG.2, the first promoter used here is different from the second
40 promoter, resulting the control of transcription by adding different RNA polymerases.
The first promoter is incorporated for aRNA amplification, whereas the second
promoter is designed for mRNA amplification. By this way in conjunction with a
reverse transcription step, we can choose to amplify aRNAs, first-strand cDNAs,
45 mRNAs or second-strand cDNAs of interest, depending on which RNA polymerase and
nuclease we use. Although the second and third preferred embodiments (FIGS.2 and 3)

5 are more complicated than the first preferred embodiment (FIG. 1), the principle and broad features of the second and third preferred embodiments are completely within the scope of the first preferred embodiment of the present invention.

10 As used herein, the first-strand complementary DNA (cDNA) refers to a DNA sequence which is complementary to a messenger RNA sequence in an A-T and C-G composition. The anti-sense RNA (aRNA) refers to a RNA sequence which is
15 complementary to a messenger RNA sequence in an A-U and C-G composition. And, the oligo(dT)-promoter sequence refers to an RNA polymerase promoter sequence coupled with a poly-deoxythymidylate (dT) sequence in its 3'-end, of which the
20 minimal number of linked dT is seven; most preferably, the number is about twenty-six. The sense sequence refers to a nucleotide sequence which is in the same sequence and composition as its homologue in mRNAs, whereas the anti-sense sequence refers to a
25 nucleotide sequence which is complementary to its respective mRNA homologue. Thus, the oligo(anti-sense polynucleotide)-promoter sequence refers to an oligonucleotide sequence which is complementary to the polynucleotide-tail of said
30 polynucleotide-tailed cDNA and also linked to an RNA polymerase promoter in its 5'-end.

35 By integrating the methods of in vitro transcription and in-cell RT-PCR (Embleton et.al., *Nucleic Acid Res.* 20: 3831-3837 (1992)), we generate the amplification cycle of the present invention. The cycle preferably starts from reverse transcription of mRNAs with Tth-like DNA polymerase, following a tailing reaction
40 with terminal transferase and then denaturation of resulting RNA-cDNA hybrid duplexes. After renaturation of above cDNAs to a specific primer or promoter primer, double-stranded cDNAs are formed by Tth-like DNA polymerase. And then, promoter-specific RNA polymerase is added to accomplish the transcriptional amplification of
45 mRNAs. The advantages of this amplification cycle of the present invention are as follows: 1) single copy mRNAs can be increased to 2000 folds in one round of amplification without mis-reading mistakes, 2) the mRNA amplification is linear and
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5 does not result in preferential amplification of abundant mRNA species, 3) the mRNA
degradation is inhibited by using fixed cells, and 4) the final mRNA products can be
10 full-length and directly used to generate a complete cDNA library.

15 In the second preferred embodiment, referring to FIG.2, when the promoter of
oligo(dT)-promoter primers is different from that of oligo(anti-sense polynucleotide)-
promoter primers, the amplification of aRNAs and mRNAs can be separated by adding
different RNA polymerases in the step (e), but not both. However, in the third
20 preferred embodiment, referring to FIG. 3, when the promoter of oligo(dT)-promoter
primers is the same as that of oligo(anti-sense polynucleotide)-promoter primers, the
amplification of aRNAs and mRNAs must be separated by adding same RNA
polymerase in the different steps, such as (e) and (h). Both preferred embodiments are
25 capable of fulfill the purpose of the present invention to amplify mRNAs from single
cells. Although we currently need to add new RNA polymerase in every round of
transcription due to the denaturation step, the finding of thermostable RNA
polymerases may make the procedure of the present invention more convenient. For
30 example, if thermostable RNA polymerases become available, the amplification cycle
can be directly completed in a microtube by following the first preferred embodiment
(FIG.1) of the present invention. Examples as mentioned here will be developed into
35 continuation in part of the present invention and is not intended in any way to limit the
broad features or principles of the present invention.

40 In stead of poly(dT), oligo(dT)-promoter, anti-sense polynucleotide and
oligo(anti-sense polynucleotide)-promoter primers, we can use sequence-specific
primers and sequence-specific promoter-linked primers to accomplish the amplification
of normalized aRNAs, mRNAs, first-strand cDNAs and second-strand cDNAs of
45 interest. The labeling of cDNAs is accomplished by incorporation of labeled
nucleotides or analogs during reverse transcription of Tth-like DNA polymerase
activity, while that of the RNAs is completed during transcription. The nucleotide
50 sequences so generated are capable of being probes in a variety of applications, such as

5 Northern blots, Southern blots, dot hybridization, in situ hybridization, position cloning,
anti-sense knock-out transfection and so on. Alternatively, the preferred embodiments
10 (FIGS. 1, 2 and 3) provide amplified full-length mRNAs for in-vitro translation. A cap-
nucleotide can be added to the 5'-end of amplified mRNAs during the transcription step
of the present invention. Unlike normalized RNAs, the capped mRNAs can be directly
15 used in protein synthesis and may help the isolation of such protein. The preferred cap-
nucleotides include P¹-5'-(7-methyl)-guanosine-P³-5'-adenosine-triphosphate and P¹-
5'-(7-methyl)-guanosine-P³-5'-guanosine-triphosphate.

20 On the other hand, the first step of the present invention can start from fixed
cells as well as mRNAs; i.e., fixed cultured cells, frozen fresh tissues, fixed tissues or
tissues in slides. Since this formed mRNAs are of full-length and carry RNA promoter
regions for in vitro/vivo expression, the transfection of certain gene transcript can be
25 directly performed after its respective double-stranded cDNA is cloned into a
competent vector. On the other hand, the present invention are also very useful in
preparing complete full-length cDNA libraries for modern gene chip technology.
30 Because the present invention is capable of generating a complete repertoire of full-
length cDNAs from single cells, tissue-specific cDNA libraries based on special cell
types can be formed and transferred onto a filter, membrane or chip for preserving these
genetic information. As we all have different genetic information from a variety of
35 major tissues and organs, the cDNA-encoded gene chips may function as an individual
source for differential screening, pathological diagnosis, physiological prognosis and
genetic identification. This kind of approach will become more and more important
40 following the completion of human genome project in the year 2003.

45 In the preferred embodiments (as shown in FIG. 1, 2 and 3) of the present
invention, according to the high amplification rate of RNA polymerase (about 2000
folds/cycle), the labor- and time-consuming factors in this RNA-PCR can be reduced to
the minimum. Also, the preparation of amplified mRNAs is cheaper and more efficient
50 than poly(dT)-linked chromatography columns in previous methods. Most importantly,

5 this RNA amplification can be carried out in microtubes with only few cells. Taken together, these special features make the content of RNA-PCR as simple, fast, and inexpensive as a kit for concisely isolating amplified mRNA sequences of interest.

10 Although certain preferred embodiments of the present invention have been described, the spirit and scope of the invention is by no means restricted to what is described above. For example, within the general framework of: a) one or more
15 specific primers for reverse transcription and polymerase extension reaction; b) one or more RNA promoter-primers for transcription; c) seven or more deoxynucleotides extended in a promoter-linked polynucleotide primer; d) seven or more same
20 nucleotides added to the 3'-end of the first-strand cDNAs; e) one or more rounds of the cycling steps for RNA amplification, there is a very large number of permutations and combinations possible, all of which are within the scope of the present invention.

EXAMPLE 1

Cell Fixation and Permeabilisation

30 LNCaP cells, a prostate cancer cell line, were grown in RPMI 1640 medium supplemented with 2% fetal calf serum. One 70% full of cells cultured in 60mm dish
35 were trypsinized, collected and washed three times in 5ml phosphate buffered saline (PBS, pH 7.2) at room temperature, then suspended in 1ml of ice-cold 10% formaldehyde solution in 0.15M NaCl. After one hour incubation on ice with
40 occasional agitation, the cells were centrifuged at 13,000rpm for 2 min and wash three times in ice-cold PBS with vigorous pipetting. The collected cells were resuspended in 0.5% Nonidet P40 (NP40, B.D.H.) and incubated for one hour with frequent agitation.
45 After that, three washes were given to cells in ice-cold PBS containing 0.1M glycine and the cells were resuspended in 1ml of the same buffer with vigorous pipetting in order to be evenly separated into small aliquots and stored at -70°C for up to a month.

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EXAMPLE 2

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First Reverse Transcription and Polynucleotide**Tailing of The First-Strand cDNAs**

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For first reverse transcription of mRNAs in cells, one hundred of the fixed cells were thawed, resuspended in 20 μ l of DEPC-treated ddH₂O, mixed with 25pmol oligo(dT)-T7 promoter (SEQ ID.1), heated to 65°C for 5 min and then cooled on ice. A 50 μ l RT reaction was prepared, comprising 10 μ l of 5x Mg-containing RT buffer (Boehringer Mannheim), 2mM dNTPs, RNase inhibitor and above cooled cells. After C. therm. polymerase (5U) was added, the RT reaction was mixed and incubated at 55°C for 10 min and shifted to 72°C for one hour, and then the cells were washed once with PBS and resuspended in a 50 μ l tailing reaction, comprising 2mM dGTP, 10 μ l of 5x tailing buffer (250mM KCl, 50mM Tris-HCl, 8mM MgCl₂, pH 8.3 at 20°C). The tailing reaction was heated at 94°C for 3 min and then chilled in ice for mixing with terminal transferase (20U), following further incubation at 37°C for 20 min. This formed said polynucleotide-tailed first-strand cDNAs.

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EXAMPLE 3

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**Denaturation, Double-Stranded cDNA Synthesis
and Transcriptional Amplification**

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Above tailing reaction was stooped at 94°C for 2 min, mixed with 25pmol poly(dC) primer (SEQ ID.2), and denatured at 94°C for 3 more min. After 1 min centrifuging at room temperature, 1mM dNTPs and C. therm. polymerase (5U) were added to form double-stranded cDNAs at 70°C for 5 min. To increase the amount of desired RNAs, the T7 promoter-linked first-strand cDNA was served as a coding strand

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5 for the transcription of T7 RNA polymerase (Eberwine et.al. (1992)). As few as several
cells in 5µl of above resulting reaction can be used to accomplish full-length aRNA
amplification during following reaction. A transcription reaction (50µl) was prepared,
10 containing 5µl of 10x transcription buffer (Boehringer Mannheim), 2mM rNTPs, RNA
inhibitor and T7 RNA polymerase (2000U). After three hour incubation at 37°C, the
cDNA transcripts were isolated from both cells and supernatant, and can be directly
15 used in following reverse transcription. The reaction was finally stopped at 94°C for 3
min and chilled in ice immediately.

20 EXAMPLE 4

Second Reverse Transcription, Denaturation,

Double-Stranded cDNA Synthesis and mRNA

Amplification

25 A 50µl RT reaction was prepared, comprising 10µl of 5x Mg-containing RT
buffer (Boehringer Mannheim), 25pmol oligo(dC)-SP6 promoter primer (SEQ ID.3),
2mM dNTPs, RNase inhibitor and 5µl of above aRNA-containing supernatant. After
30 C. therm. polymerase (5U) was added, the RT reaction was mixed and incubated at
55°C for 10 min and shifted to 72°C for one hour. This formed said second-strand
cDNAs. After another denaturation at 94°C for 3 min and mixing with 25pmol
poly(dT) primer (SEQ ID.4) at room temperature for 1 min, double-stranded cDNAs
35 can be formed by adding 1mM dNTPs at 70°C for 5 min. A transcription reaction
(50µl) was then prepared to generate said amplified mRNAs, containing 5µl of 10x
transcription buffer (Boehringer Mannheim), 2mM rNTPs, RNA inhibitor and SP6
40 RNA polymerase (2000U). After three hour incubation at 37°C, the cDNA transcripts
were isolated and can be directly used in another round of RNA-PCR. The final
reaction was stopped at 94°C for 3 min and chilled in ice immediately.. The quality of
45 final amplified mRNAs (2µg) was assessed on a 1% formaldehyde-agarose gel, ranging
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5 from 500 bp to above 10kb (FIG.4a). We also have successfully identified the gene
transcripts of RB, p21, β -actin and GAPDH on the Northern blots of full-ranged
LNCaP mRNAs made by the present invention (FIG.4b).

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The present invention has been described with reference to particular preferred
embodiments; however, the scope of this invention is defined by the attached claims
15 and should be constructed to include reasonable equivalents.

20 Defined in detail, the present invention is a polymerase chain reaction method of
generating amplified messenger RNAs from single cells, comprising the steps of:

- 25 a. providing a plurality of messenger RNAs for following steps;
- b. contacting said messenger RNAs with a plurality of first primer sequences
to form a plurality of first-strand complementary DNAs, wherein said first-
strand complementary DNAs are generated by reverse transcription of said
30 messenger RNAs with said first primers;
- c. permitting terminal extension of said first-strand complementary DNAs to
form a plurality of polynucleotide-tailed first-strand complementary
35 DNAs, wherein said polynucleotide-tailed first-strand complementary
DNAs are tailed by multiple copies of deoxynucleotides;
- 40 d. incubating denatured said polynucleotide-tailed first-strand
complementary DNAs with a plurality of second promoter-containing
primers to form a plurality of double-stranded complementary DNAs,
45 wherein said double-stranded complementary DNAs are generated by
extension of DNA polymerase activity;

- 5
- e. permitting transcription of said double-stranded complementary DNAs to
form a plurality of amplified messenger RNAs, wherein said amplified
10 messenger RNAs are generated by extension of RNA polymerase activity
through the promoter region of said double-stranded complementary
DNAs; and
- 15 f. contacting said amplified messenger RNAs with said first primer
sequences to form a plurality of said polynucleotide-tailed first-strand
complementary DNAs, wherein said polynucleotide-tailed first-strand
20 complementary DNAs are generated by reverse transcription of said
amplified messenger RNAs.

25 Defined broadly, the present invention is an RNA amplification method of
performing improved messenger RNA enrichment, comprising the steps of:

- a. providing a plurality of messenger RNAs for following steps;
- 30 b. generating a plurality of polynucleotide-tailed complementary DNAs from
said messenger RNAs, wherein said polynucleotide-tailed complementary
DNAs are reverse-transcribed from said messenger RNAs and tailed by
35 multiple copies of deoxynucleotides;
- c. permitting denatured said polynucleotide-tailed complementary DNAs to
form a plurality of double-stranded complementary DNAs, wherein said
40 double-stranded complementary DNA contains a complementary DNA
sequence flanked with an RNA polymerase promoter and a
polynucleotide-tail; and
- 45 d. incubating said double-stranded complementary DNAs in a plurality of
promoter- and primer-dependent extension systems, and thereby providing
50 a plurality of amplified messenger RNAs from said messenger RNAs.

5 Of course the present invention is not intended to be restricted to any particular
form or arrangement, or any specific embodiment disclosed herein, or any specific use,
10 since the same may be modified in various particulars or relations without departing
from the spirit or scope of the claimed invention hereinabove shown and described of
which the apparatus shown is intended only for illustration and for disclosure of an
operative embodiment and not to shown all of the various forms or modifications in
15 which the present invention might be embodied or operated.

The present invention has been described in considerable detail in order to
20 comply with the patent laws by providing full public disclosure of at least one of its
forms. However, such detailed description is not intended in any way to limit the broad
features or principles of the present invention, or the scope of patent monopoly to be
25 granted.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 4

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCAGTGAATT GTAATACGAC TCACTATAGG GAATTTTTTT
TTTTTTTTTT TTTTTT

5

(2) INFORMATION FOR SEQ ID NO:2:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCCCCCCC CCCCCC

18

25

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic"

35

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

40

CCATATGGCA TTAGGTGAC ACTATAGAAG CCCCCCCCCC C

41

(2) INFORMATION FOR SEQ ID NO:4:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid

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(A) DESCRIPTION: /desc = "synthetic"

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTTT TTTTTTTTTT TTTTTT

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Claims

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WHAT WE CLAIM IS:

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1. A method of generating amplified messenger RNAs with polymerase reaction activity, comprising the steps of:

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- a. providing a plurality of messenger RNAs for following steps;
- b. contacting said messenger RNAs with a plurality of first primer sequences to form a plurality of first-strand complementary DNAs, wherein said first-strand complementary DNAs are generated by reverse transcription of said messenger RNAs with extension of said first primers;
- c. permitting terminal extension of said first-strand complementary DNAs to form a plurality of polynucleotide-tailed first-strand complementary DNAs, wherein said polynucleotide-tailed first-strand complementary DNAs are tailed by multiple copies of deoxynucleotides;
- d. incubating denatured said polynucleotide-tailed first-strand complementary DNAs with a plurality of second promoter-containing primers to form a plurality of double-stranded complementary DNAs, wherein said double-stranded complementary DNAs are generated by extension of DNA polymerase activity with said second promoter-containing primers;
- e. permitting transcription of said double-stranded complementary DNAs to form a plurality of amplified RNAs, wherein said amplified RNAs are generated by extension of RNA polymerase activity through the promoter region of said double-stranded complementary DNAs; and
- f. contacting said amplified RNAs with said first primer sequences to form a plurality of said polynucleotide-tailed first-strand complementary DNAs, wherein said polynucleotide-tailed first-strand complementary DNAs are

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generated by reverse transcription of said amplified RNAs with extension of said first primer sequences.

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2. The method as defined in Claim 1, further comprising repeated steps (d) through (f) at least one time.

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3. The method as defined in Claim 1, further comprising the step of cell fixation for preventing intracellular RNA degradation before the step (a).

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4. The method as defined in Claim 1, further comprising the step of cloning said double-stranded complementary DNAs into competent vectors after the step (f).

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5. The method as defined in Claim 1, further comprising the step of incorporating a plurality of cap-nucleotides into 5'-ends of said amplified messenger RNAs for in vitro translation in the step (e).

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6. The method as defined in Claim 5, wherein said cap-nucleotide is selected from the group consisting of P¹-5'-(7-methyl)-guanosine-P³-5'-adenosine-triphosphate; P¹-5'-(7-methyl)-guanosine-P³-5'-guanosine-triphosphate, P¹-5'-(7-methyl)-guanosine-P³-5'-cytidine-triphosphate and P¹-5'-(7-methyl)-guanosine-P³-5'-uridine-triphosphate.

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7. The method as defined in Claim 1, wherein said reverse transcription is an enzyme activity selected from the group consisting of AMV, M-MuLV, HIV-1 reverse transcriptase and Tth-like DNA polymerase with reverse transcription activity.

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8. The method as defined in Claim 7, wherein said enzyme activity is performed at temperature ranged from about 37°C to about 80°C.

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9. The method as defined in Claim 1, wherein said first primer sequences are complementary to the tails of said messenger RNAs.

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- 5 10. The method as defined in Claim 9, wherein said first primer sequences are coupled to an RNA polymerase promoter and contain about eight to about thirty copies of deoxythymidylates.
- 10 11. The method as defined in Claim 1, wherein said denatured polynucleotide-tailed first-strand complementary DNAs are formed at temperature ranged from about 90°C to about 100°C.
- 15 12. The method as defined in Claim 1, wherein said DNA polymerase activity is an enzyme activity selected from the group consisting of E. coli DNA polymerase 1, Klenow fragment of E. coli DNA polymerase 1, T4 DNA polymerase, Taq DNA polymerase, Pwo DNA polymerase, Pfu DNA polymerase and Tth-like DNA polymerase, C. therm. polymerase.
- 20 13. The method as defined in Claim 12, wherein said DNA polymerase activity is achieved by Tth-like DNA polymerase with reverse transcriptase activity.
- 25 14. The method as defined in Claim 12, wherein said DNA polymerase activity is performed at temperature ranged from about 35°C to about 85°C.
- 30 15. The method as defined in Claim 1, wherein said second promoter-containing primers are oligonucleotide sequences complementary to the polynucleotide tails of said polynucleotide-tailed first-strand complementary DNAs and also coupled to an RNA polymerase promoter for transcription activity in the step (e).
- 35 40 16. The method as defined in Claim 15, wherein said RNA polymerase promoter is selected from the group consisting of T3, T7, SP6 and M13 RNA polymerase promoter.
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- 5 17. The method as defined in Claim 1, wherein said transcription is an RNA polymerase activity selected from the group consisting of T3, T7, SP6 and M13 RNA polymerase.
- 10 18. The method as defined in Claim 17, wherein said RNA polymerase activity is performed at temperature ranged from about 35°C to about 85°C.
- 15 19. The method as defined in Claim 18, wherein said RNA polymerase activity is performed at about 37°C.
- 20 20. The method as defined in Claim 1, wherein said polynucleotide-tailed first-strand complementary DNAs are tailed by terminal extension activity selected from the group consisting of terminal transferase and AMV reverse transcriptase with multiple copies of same kind of deoxynucleotides.
- 25 21. The method as defined in Claim 20, wherein said same deoxynucleotide is selected from the group consisting of deoxyguanylate, deoxycytidylate, deoxyadenylate, deoxythymidylate and deoxyuridylate.
- 30 22. A method of performing improved messenger RNA amplification, comprising the steps of:
- 35 a. providing a plurality of messenger RNAs for following steps;
- b. generating a plurality of polynucleotide-ended complementary DNAs from said messenger RNAs, wherein said polynucleotide-ended complementary DNAs are reverse-transcribed from said messenger RNAs and tailed by multiple deoxynucleotides in the ends;
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- 45 c. permitting denatured said polynucleotide-tailed complementary DNAs to form a plurality of double-stranded complementary DNAs, wherein said double-stranded complementary DNAs contain a complementary DNA
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sequence flanked with an RNA polymerase promoter and a polynucleotide-tail; and

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- d. incubating said double-stranded complementary DNAs in a plurality of promoter- and primer-dependent extension systems, and thereby providing a plurality of amplified RNAs from said messenger RNAs.

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23. The method as defined in Claim 22, further comprising repeated steps (b) through (d) at least one time

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24. The method as defined in Claim 22, further comprising the step of cloning the double-stranded complementary DNAs of said amplified messenger RNAs into competent vectors after the step (d).

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25. The method as defined in Claim 22, wherein said messenger RNAs are protected by fixation.

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26. The method as defined in Claim 22, wherein said messenger RNAs are protected by a plurality of RNase inhibitors.

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27. The method as defined in Claim 22, further comprising the step of incorporating a plurality of cap-nucleotides into 5'-ends of said amplified messenger RNAs for in vitro translation in the step (d).

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28. The method as defined in Claim 27, wherein said cap-nucleotide is selected from the group consisting of P¹-5'-(7-methyl)-guanosine-P³-5'-adenosine-triphosphate, P¹-5'-(7-methyl)-guanosine-P³-5'-guanosine-triphosphate, P¹-5'-(7-methyl)-guanosine-P³-5'-cytidine-triphosphate and P¹-5'-(7-methyl)-guanosine-P³-5'-uridine-triphosphate.

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29. The method as defined in Claim 22, wherein said complementary DNAs are reverse-transcribed by an enzyme activity selected from the group consisting of

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AMV, M-MuLV, HIV-1 reverse transcriptase and Tth-like DNA polymerase with reverse transcription activity.

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30. The method as defined in Claim 22, wherein said RNA polymerase promoter is selected from the group consisting of T3, T7, SP6 and M13 RNA polymerase promoter.

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31. The method as defined in Claim 22, wherein said polynucleotide-tailed complementary DNAs are formed by terminal extension activity selected from the group consisting of terminal transferase and AMV reverse transcriptase.

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32. The method as defined in Claim 22, wherein said promoter- and primer-dependent extension systems are a plurality of mixed polymerase activities containing RNA polymerase, DNA polymerase and reverse transcriptase.

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33. The method as defined in Claim 32, wherein said mixed polymerase activities are selected from the group consisting of T3, T7, SP6, M13 RNA polymerases and Tth-like DNA polymerase with reverse transcriptase activity, *C. therm.* polymerase.

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34. The method as defined in Claim 22, wherein said polynucleotide-tailed complementary DNAs are tailed by terminal extension with multiple copies of same deoxynucleotides.

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35. The method as defined in Claim 34, wherein said same deoxynucleotide is selected from the group consisting of deoxyguanylate, deoxycytidylate, deoxyadenylate, deoxythymidylate and deoxyuridylate.

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36. The method as defined in Claim 34, wherein said terminal extension is an enzyme activity selected from the group consisting of terminal transferase and AMV reverse transcriptase.

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FIG.1

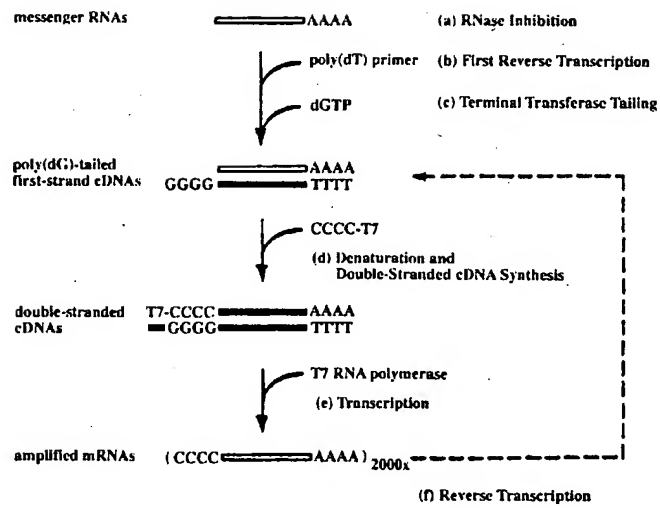


FIG.2

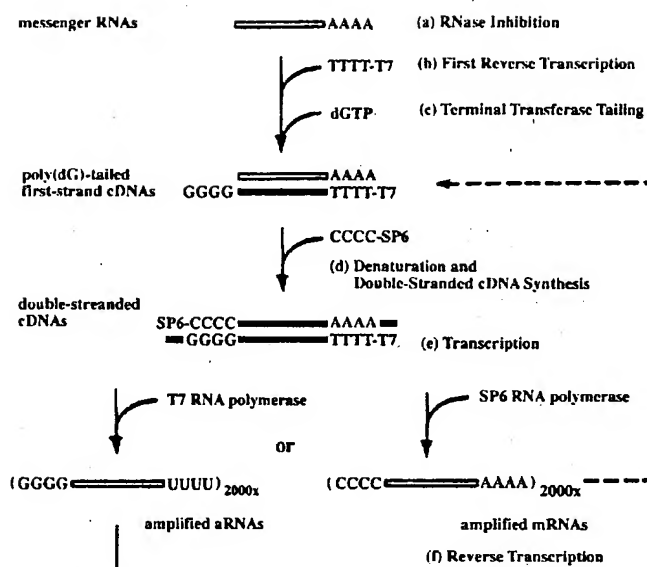


FIG.3

FIG.3

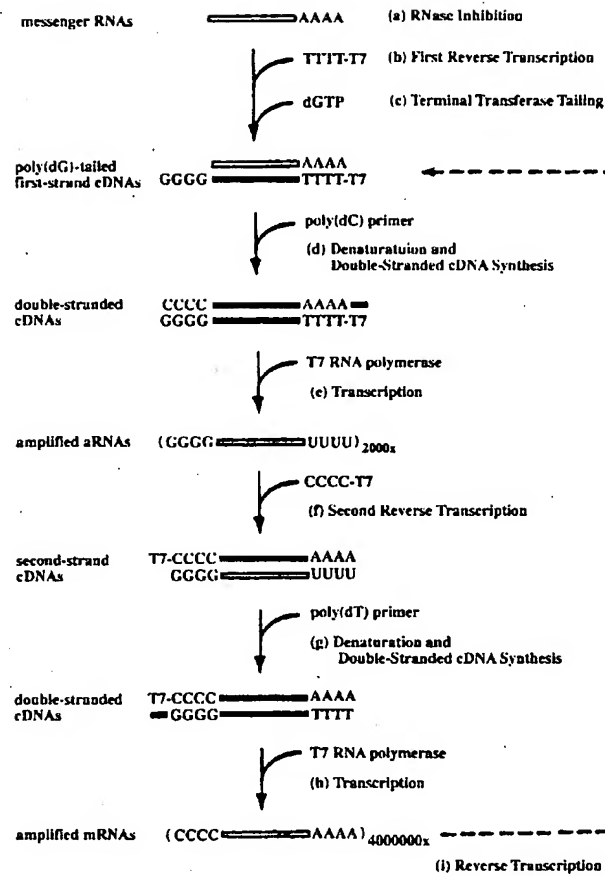


FIG.4(a)

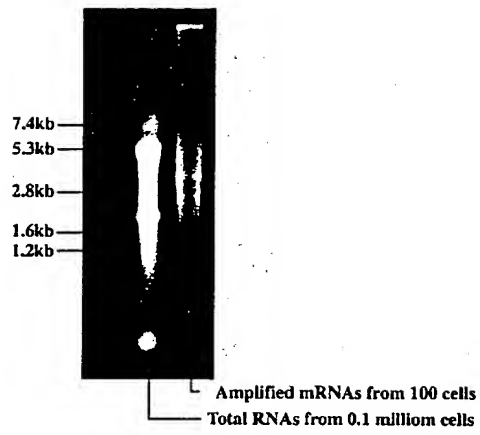
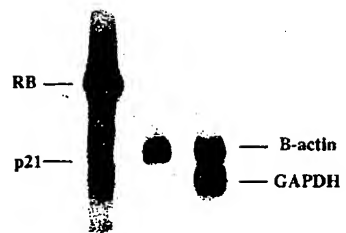


FIG.4(b)



INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/12461

A. CLASSIFICATION OF SUBJECT MATTER IPC(6) : C12P 19/34; C07H 21/02 US CL : 435/91.1, 91.2; 536/23.1 According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 435/91.1, 91.2; 536/23.1 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) WEST, STN MEDLINE, CAPLUS, terms, amplif? messenger RAN/mRNA, RNA PCR, RT-RNA		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 5,501,963 A (BURCKHARDT) 26 March 1996, see entire document.	1-36
A	US 5,599,672 A (LIANG et al) 04 February 1997, see entire document.	1-36
A	US 5,665,547 A (PARDEE et al) 09 September 1997, see entire document.	1-36
<input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* Special categories of cited documents:		
A document defining the general state of the art which is not considered to be of particular relevance	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention	
B earlier document published on or after the international filing date	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone	
L document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art	
O document referring to an oral disclosure, use, exhibition or other means	*A* document member of the same patent family	
P document published prior to the international filing date but later than the priority date claimed		
Date of the actual completion of the international search 05 NOVEMBER 1999	Date of mailing of the international search report 02 DEC 1999	
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